

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2000, 10:14:55 ; Search time 10069.4 Seconds
(without alignments)
3256.749 Million cell updates/sec

Title: US-09-227-881-2

Perfect score: 5304

Sequence: 1 atcttggtcagttacctc.....caggcacctcagcacagc 5304

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
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20: gb_est20:*
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110: gb_gss19:*
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112: gb_gss21:*
113: gb_gss22:*
114: gb_gss23:*
115: gb_gss24:*
116: em_gss5:*
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DNA sequence.
ACCESSION AQ379787.1 GI:4350810
VERSION AQ379787.1
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..539
/organism="Homo sapiens"
/db_xref="GDB:7558034"
/db_xref="taxon:9606"
/clone="RPCI-11-152C3"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 187 a 112 c 123 g 116 t 1 others
ORIGIN
Query Match 3.4%; Score 179.8; DB 96; Length 539;
Best Local Similarity 76.8%; Pred. No. 3.6e-21;
Matches 235; Conservative 0; Mismatches 63; Indels 8; Gaps 1;
OY 1280 agggtagaggtctgtctctacacacctgctgtctctacacctgagctcactgcaacc 1339
DB 327 AGAGTCTCGCTGTCTACNCAGGCTGAGTTCAGTGGCGGAGTCTGGGCTCAGTCCAGC 268
OY 1340 tctgacctccagggtctcaagaattctctctctcctcagacctcccggtctgagtgagctacag 1399
DB 267 TCGGCTCCCGGGGTCAAGCAATTCCTGCTCAGCTCCCGAGTGTGCGGAGCAGCAG 208
OY 1400 gc-----gcaagcccgagctaatcttctgtatctgttaagtagagagatggggtttacata 1451
DB 207 GCATGTGCCACCAATACCGCGCTAATTTTGTATTAGTAGAAGAACGCGGTTTCACCATG 148
OY 1452 ttggaccgagtgctctgaaacctctcagctcagtgatgacacacacctcagccctccaaa 1511
DB 147 TTGGCCAGGCTGGCTTGAATCTCTGACCTCAGGTGATCCACGAGCTTGGCTCTCTAAA 88
OY 1512 gtctcgagattacagcatagtagtaaccgagcccgagccaaggtctgagtgatgagtgagaa 1571
DB 87 GTGTGGGATTTACAGACAGTGTACACACGCGCGCTCAATCCTTTTATACAGCTA 28
OY 1572 caactt 1577
DB 27 TGAATT 22

RESULT 3
LOCUS AQ636457/c 645 bp DNA GSS 17-JUN-1999
DEFINITION RPCI-11-465121.TU RPCI-11 Homo sapiens genomic clone RPCI-11-465121
, DNA sequence.
ACCESSION AQ636457
VERSION AQ636457.1 GI:5099092
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 645)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..645
/organism="Homo sapiens"
/db_xref="GDB:7678388"
/db_xref="taxon:9606"
/clone="RPCI-11-465121"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT 214 a 118 c 139 g 174 t
ORIGIN
Query Match 3.4%; Score 179; DB 100; Length 645;
Best Local Similarity 88.2%; Pred. No. 4.8e-21;
Matches 209; Conservative 0; Mismatches 20; Indels 8; Gaps 1;
OY 1322 cctgagctcactgcaacctctgctccccaaggtcaagcaattctctgtctcagctccc 1381
DB 248 CTTCAGCTCACTCAACCTCTGCTCCAGAGTCAAGTAATTCCTGCTCAGCTCC 189
OY 1382 gcgtagctgagctacaggg-----caagccggcgcaattttgtgtgttagtag 1433
DB 188 GAGTAGCTGGGATTACAGGGCTGTGTACACCGCCAGCTAATTTTGTATTAGTAG 129
OY 1434 agatgggggttccaccatattagcccgagctgtctgaaacctcagacctcagtgatccac 1493
DB 128 AGATGGGATTTCACATAGTTGGCCAGAGCTGTCTCGACTCTCGACTCAAGTGAATGTC 69
OY 1494 ccacctcagctcttaagtgctgggattacagagcatgagtagtcaacgagccggccaa 1550
DB 68 CCACCTCAGCTCCCAAGAGTGTGGATTACAGCATGACACACCGCGCGCCGCCAA 12
RESULT 4
LOCUS AQ387027/c 678 bp DNA GSS 21-MAY-1999
DEFINITION RPCI11-153C12.TU RPCI-11 Homo sapiens genomic clone RPCI-11-153C12,

ACCESSION	DNA sequence.
VERSION	A0387027
KEYWORDS	GC
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. Zhuo,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.
TITLE	Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Other GSSs: RPCI1-153C12.TV Contact: Shaying Zhuo, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pietere@jorg.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html Seq primer: Sp6 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..678 /organism="Homo sapiens" /db_xref="GDB:7558427" /ab_xref="taxon:9606" /clone="RPCI-11-153C12" /clone_11b="RPCI-11" /sex="Male" /cell_type="Lymphocytes" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
BASE COUNT	210 a 151 c 171 g 146 t
ORIGIN	
Query Match	3.4% Score 179; DB 96; Length 678;
Best Local Similarity	77.4%; Pred. No. 4.7e-21;
Matches 233:	Conservative 0; Mismatches 60; Indels 8; Gaps 1;
OY 1274	tccgtgagggtgaagtgctgtgtcttacacctactcgtatgtcttaaccctgagtctact 1333
Db 364	TCAGACAGAGTCTTGCTCTCGTCGTCAAGCTGGAAGCAATGGACAGACTCGGCTCACT 305
OY 1334	gcaacctctgcctcccagaagttcaagaacattccctcgcttcacaagcccccgagctggga 1393
Db 304	GCAACCTCCGCCCTCCAGAGTTCAACAATTCCTGCGCTCACCCCTCCCATGTAGCTGGGA 245
OY 1394	ctacagagc-----gcacgccgcgcctaatttgttatgttagtagagatggggttc 1445
Db 244	TTTAGCGGACACCACACACCATGCCCCGGCTAATTTTTTTATTATTAGTAGAGTGGGTTTC 185
OY 1446	accacatatagcccgagctgtgtcttgaaactcctgaactcaggtgatccaccacccaagcct 1505
Db 184	ACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGTGATGATCGCCCGCTTAGCCT 125
OY 1506	cctaagaagctggagattacagagcatgagtcaacgcgcgcgcgcgaagggatcagtgtttaat 1565
Db 124	CCCAAGAAGTGTGGGATTAACAGCGCTGAGGACACCGCGCCGCTTTATTTATTTTATG 65
OY 1566	a 1566
Db 64	A 64

RESULT	5
LOCUS	AM978041
DEFINITION	EST390150 MAGE cDNA sequence.
VERSION	AM978041
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 537)
TITLE	Heide,P., Ol,R., Abernathy,K., Dharap,S., Gasparid,R., Gay,C., Holt ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J. Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: john@glfr.org Plate: 387 Seq primer: Forward.
JOURNAL COMMENT	Location/Qualifiers 1..537 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_id="MAGE ressequences, MAGO" /note="Vector: pBluescriptSm"
BASE COUNT	119 a 157 c 141 g 118 t 2 others
ORIGIN	
Query Match	3.4%; Score 178.4; DB 25; Length 537;
Best Local Similarity	77.2%; Pred. No. 6.2e-21;
Matches 233; Conservative	0; Mismatches 61; Indels 8; Gaps 1
OY	1281 gggtgagggctcgtgtcttaccacccactcgttgtcttcacctgaagcttcgaacct 1340
DB	6 GAGTGTGCTCGTTGGCCACGCGTAGTGCAATGCATGATCTCGCTCACCAGCAACT 65
OY	1341 cygcctccaggttcaagaattccctcgttcacagcctcccgtagctcgagactacagg 1400
DB	66 CCACCTCCCAGTAATTAAAGGAGATTCTTCCTGCCCTCACGCTCCGAGTAGCTGGGATTACAG 125
OY	1401 cg-----cagcccgagtaatttttgatttgttagtagagatggggttcaccatat 1452
DB	126 TGCCCCACACACACACCGCATATTTTTGTATTTTAGAAGAATGGCGTTCCACCATAT 185
OY	1453 tagcccgagctgtgtcttgaaactctgaacctcaagtgatcacccacactgaagcttcctaag 1512
DB	186 TGGCCAGACTGGCTTCGAACCTCTCACTCAAGTAGATCCACCCTCAGCTCCACAG 245
OY	1513 tgctgagattacaagcatagctacagcgccccgccaagtgtagtcttaaagaagt 1572
DB	246 TGCTGGGATTATAGCGCTGAGCCACCGCCGCGCTTGAGAACAGTCTTTAAAGSAGG 305
OY	1573 aa 1574
DB	306 AA 307
RESULT	6
LOCUS	AQ112451
DEFINITION	CIT-HSP-2372C9.1F CIT-HSP Homo sapiens genomic clone 2372C9, DNA sequence.
ACCESSION	AQ112451
VERSION	AQ112451.1 GI:3484611

KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 516) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other GSSs: CIT-HSP-2372C9.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/Bac_end_search/Bac_end_search.html . Seq primer: M3-21 Class: BAC ends.
FEATURES	Location/Qualifiers
source	1..516 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2372C9" /clone_11b="CIT-HSP" /sex="Male" /cell_type="Sperm" /note="Vector: pBelobaC11; Site_1: HindIII; Site_2: HindIII"
BASE COUNT	87 a 145 c 118 g 166 t
ORIGIN	
Query Match	3.3%: Score 177.6; DB 89; Length 516;
Best Local Similarity	85.2%: Pred. No. 8.6e-21;
Matches 213; Conservative	0; Mismatches 29; Indels 8; Gaps 1
OY	1321 accctgagctactgcaacctctgctctcccaaggttcaagcaattctctgctcaagctcc 1380
Db	255 ATCTACGCTACCTACGCAACTCTGCTCCGCGGTTCAAGCGATTCCTCGTACGCTCC 314
OY	1381 cgcgcagctcgggaactcaggcg-----caagcccgctaatatttgcattgttgta 1432
Db	315 CAAGTAGCTGGGATTACAGGCGCACACACACAGCCCGGCTAATTTTGTATTTTAA 374
OY	1433 gagaatggaggttccacatatgagccggctggtcttgaaactctgaccccaagtgatca 1492
Db	375 GAGATGGGGTTTACCATGTTGGCCAGCGTGTCTGCACTCTGACCTTAAGTATCA 434
OY	1493 ccacactcagcctctcaagaagtctgggattacacagcatgtagtaccgcgcggcccaag 1552
Db	435 CCCACTTGCTGCTCCCAAGTGTGGGATTACAGGCGCTGGCGCACTGCGCCAGCCTAAT 494
OY	1553 gtcaagtgttt 1562
Db	495 TTTCGATTT 504
RESULT 7	
LOCUS	A0265389 577 bp DNA GSS 27-OCT-1998
DEFINITION	CITBI-EI-2509010.TF CITBI-EI Homo sapiens genomic clone 2509010, DNA sequence.
ACCESSION	A0265389
VERSION	A0265389.1 GI:3793589
KEYWORDS	GSS.
SOURCE	human.

ORGANISM	Homo sapiens		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.		
TITLE	Use of a random human BAC End Sequence Database for Sequence-Ready Map Building		
JOURNAL	Unpublished (1998)		
COMMENT	Other_GSSs: CIBI-EI-2509010.TR Contact: Mark Adams The Institute of Eukaryotic Genomics Department of Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (Info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html. Seq primer: M13-21 Class: BAC ends.		
FEATURES	Location/Qualifiers		
source	1..577 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="2509010" /clone_1lb="CIBI-EI" /sex="male" /cell_type="sperm" /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; Caltech Human BAC Library D"		
BASE COUNT	167 a 127 c 137 g 146 t		
ORIGIN			
Query Match	3.3%; Score 177.4; DB 91; Length 577;		
Best Local Similarity	75.1%; Pred. No. 9.1e-21;		
Matches 238; Conservative	0; Mismatches 71; Indels 8; Gaps 1		
Oy	1321	acctgagctcactgcaacctcgtccctccaggcttaagcaattctctctgctcagctcc	1380
Db	368	atctcggctcactgcaacctcgtccctccaggcttaagcaattctctcctcagctcc	309
Oy	1381	cgcgtgagctgagctacacagc-----gcacgcgccgctaatcttctgattgttagta	1432
Db	308	cgagatattctagacatcacagcacccgccacacagcctgctatttttgcatttttttagta	249
Oy	1433	gagatggggtttcacacatactagccgcgctggtccttgaaacctccgacctcaggtgacaa	1492
Db	248	gagagcggggtttcacacattggtgtgcagcctggtctgaactcctgacctcagcgatcaca	189
Oy	1493	cccacctcagcctcctctaaagtctctggtatataagsgatgaatgcacccgcgcgcgccaag	1552
Db	188	cccccttggcctccccaagtgctgggattgaagcattagcctacacccagccacga	129
Oy	1553	gtcagtgatttaataaggaataacttgaatggttacttaacaacacaggaagaacagacaa	1612
Db	128	gattacatttttttaattctagacctgagactgacatggcacacactctctcagcgaaggaat	69
Oy	1613	agctgtgataatttcag	1629
Db	68	agtaatactggtatgag	52
RESULT	8		
LOCUS	AI583291		
DEFINITION	AI583291 548 bp mRNA EST 14-DEC-1999		
ACCESSION	U556902.x1 NC1 CGAP HSC4 Homo sapiens cDNA clone IMAGE:2244818 3'		
	similar to TR:Q13538 Q13538 ORF2: FUNCTION UNKNOWN. contains Alu		
	repetitive element, mRNA sequence.		
	AI583291		

VERSION	AI583291.1	GI:4569188
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 548)	
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .	
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Kitzman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.lnl.gov/bhrp/image/image.html Insert length: 664 Std Error: 0.00 Seq primer: -40UP from Glbco High quality sequence stop: 664 POLYA-No.	

FEATURES	SOURCE
1. .548	Location/Qualifiers
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_image="224818"
	/clone_lib="NCI_CGAP_HSC4"
	/tissue_type="CD34+ , CD38- from normal bone marrow donor"
	/lab_host="DH10B"
	/note="organ: bone marrow; Vector: pAMP1, mRNA made from lymphoid tissue, cDNA made by oligo-dT priming. directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. CDNA Library Preparation: David B. Kitzman, Ph.D. Reference: Kitzman et al. (1996) Cancer Research 56:5380-5383."
BASE COUNT	150 a 136 c 129 g 133 t
ORIGIN	

	Only Match	3.3%	Score 17.7.2	DB 11	Length 548
	Best Local Similarity	78.8%	Pred 10.9.e-21		
	Matches 227	Conservative 0	Mismatches 53	Indels 8	Gaps 1
Oy	1277	gtgagggtgaggggtctgtgtgtcttaacactaactgtatgtctcttaacactgagctactgca	1336		
Db	546	GAGGAGAGCTTGATGATGTGGCTCAGAGCTGAGAGTGCGAGTGCGATGCTTGCCCACTGGCA	487		
Oy	1337	acctctgtctcccaaggttcaagaacaattctctctgtctcaagctcccgctgaagctggagacta	1396		
Db	486	ACCTCGGCTGCACAGGTTTCACAGCATTTCTCCTGCGCCACAGCTCTCTTACGACGCTGNAAC	427		
Oy	1397	cagcgct-----cagcgccgagctaaatttttgtatgtttagtagagatggggtttcacc	1448		
Db	426	CAGGCGCCCGCCACACACAGCGCTGGCTAATTTTGTATTTTGTAGTAGAGATGGGGTTTTCACC	367		
Oy	1449	atatttagcccgagctgtgtcttgaacctcctgaacctcgaagtatcccaaccactcaagctcctc	1508		
Db	366	ATGTTGGCCAGGCTGCTGTCGAACTCTGACCTCAGAGTATCCACCCACTCTGTGTCCG	307		
Oy	1509	aaagtgtctggagattacaaggacatgaatcacgcgcgcgcgcgaaggttca	1556		
Db	306	AAAGGCTGGGATTTACAGGCATGAGCCACCGTGCAGCCACGAGATTTA	259		

RESULT	9		
AQ199435/c			
LOCUS	AQ199435	434 bp	DNA
			GSS
			20-APR-1999

DEFINITION	RPC111-58F5_TJ RPC1-11 Homo sapiens genomic clone RPC1-11-58F5, DNA sequence.
ACCESSION	A0199435
VERSION	A0199435.1
KEYWORDS	GI:3611634
SOURCE	GSS.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 434)
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE	Use of human BAC End sequences for Sequence-Ready Map Building
JOURNAL	Unpublished (1998)
COMMENT	Other-GSSs: RPC111-58F5_TK Contact: Mark Adams Department of Eukaryotic Genomes The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: madams@tigr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@jong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html Class: BAC ends.

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FEATURES
SOURCE
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="GDB:7522012"
/db_xref="taxon:9606"
/clone="RPC1-11-58f5"
/clone_11b="RPC1-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"
BASE COUNT
118 a 108 c 114 g 94 t
ORIGIN

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Query Match	3.3%	Score 176.6	DB 90:	Length 434:
Best Local Similarity	77.4%	Pred. No. 1.3e-20:		
Matches 230:	Conservative 0:	Mismatches 59:	Indels 8:	Gaps 1:
Qy 1292	tgctgttaacacccctacccgtgatgctctctacaccctagacacacctgtcaacacctgctccccag	1351		
Db 427	TGTCACTAAGGCTGGAGTGTGCAATGGCACGATCTTGGCTCTGTGCAACCTCTGCTCTCGG	368		
Qy 1352	gtccacgaattctctctgtccacagcctcccgctagctctggagactacagc-----gc	1403		
Db 367	GTTCAAGAATTCTCTCTGTCTCAGCTCTCCAAATGATGAGATTACAGGACACGGCCAAAC	308		
Qy 1404	acgccccgagtaattctgtatctgtatagatagatggggttcacacataatagcccgctg	1463		
Db 307	ATGCCCGCATATTTTGTATTTTATTTAGTACAGATGGGGTTTCACTATTTGGCTTGCTGA	248		
Qy 1464	gtcttgaacctctgaacctcaagtgatccacccacctcaagcctctctaaagtctggtgata	1523		
Db 247	GTCCTGAACCTCCGGACACCTCAGAGTATCCACTGCTTGCCCTCCTGAACTCTGGATTA	188		
Qy 1524	caggcatgagtcacacgcggcccgccgaaggtcagtggttaataaggaataactggaa	1580		
Db 187	CAGGTGTGATGCTACCCGTCTCCAGCCAGGATGATGGGTTTATTCAGGAAGATCTGAA	131		

RESULT	10
AM979191	
LOCUS	AW979191
DEFINITION	591 bp mRNA EST EST3391301 MAGE resequences, MAGP Homo sapiens cDNA, mRNA sequence.

ACCESSION	AW979191	GI:8170478
VERSION	AW979191.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 591)	
AUTHORS	Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and Quackenbush,J.	
TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208 Email: johnget@igr.org Plate: 403 Seq primer: Forward.	
FEATURES	Location/Qualifiers	
source	1..591 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MAGE sequences, MAGP" /note="Vector: pBluescriptSm"	
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Query Match	3.3%; Score 176.6; DB 25; Length 591;	
Best Local Similarity	71.9%; Pred. No. 1.2e-20;	
Matches 248; Conservative	0; Mismatches 89; Indels 8; Gaps 1;	
Oy	1281 gggtagaggtcgtgtctctacaccctaccctgtgtctctacactgagtcctcatgcaact	1340
Db	132 GAGTGTTCGTCTGTACCCAGGCTGAAGTGCAGTGGCACAAATCTGGCTCAGTCGAACTT	191
Oy	1341 cgcctccagggtcaagaacatctccgtctccagcctccgcgtagctgtgactacaag	1400
Db	192 CCACCTCCCAAGTTTAAGCAATTCCTGTCTCAGCCTCTTAAGTAGCTGGAGACTRGAAG	251
Oy	1401 cgcacg-----ccgcgctaattcttgatctgttagtagagatgagggttaccatat	1452
Db	252 GGGCCGCCACATACCAAGCTAATTTTCTATTATTAGTAGAGATGGGCTTCACCATAT	311
Oy	1453 tagcccgctgtgtcttgaactcctcaactcaagtgatcacccacactcaagctctctaag	1512
Db	312 TGGTCAAGCTGTCTTGAACCTCTCAACCTCAAGTGTATCCACCGCTTGCCCTCCCAAG	371
Oy	1513 tgcctggattaaaggcattagatgcacgcgcgcgcgcgaaggtcagtggttaataaggaat	1572
Db	372 TGCTGGGATGACAGCGGTGAGCCACTGCCCCAGCCACAAGTTCTGGAAATTTTAAGCCA	431
Oy	1573 aacttgaatgttactaaaccaacacagaggaaacagacaaagctg 1617	
Db	432 AATATTAATCTATTTAACACTCAATGCGCATTACTCAACAGAAATG 476	
RESULT 11		
LOCUS	AW273360 521 bp mRNA EST 03-JAN-2000	
DEFINITION	x13804.x1 NCI_GCAP_v14 Homo sapiens cDNA clone IMAGE:2762382 3'	
ACCESSION	AW273360	
VERSION	AW273360.1	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	I. (bases 1 to 521)
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Gene distribution: NCI-CGAP clone distribution Information can be found through the I.M.A.G.E. Consortium/LINL at: www.bio.linnl.gov/bdrip/image/image.html
FEATURES	Possible reversed clone: polyT not found Seq primer: -40UP from gibco High quality sequence stop: 411. Location/Qualifiers
SOURCE	1..521 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2762382" /clone_1lb="NCI_CGAP_Uc4" /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors" /lab_host="DH10B" /note="Organ: uterus; Vector: PCMV-SPOrt6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"
BASE COUNT	115 a 131 c 108 g 167 t
ORIGIN	
Query Match	3.3%; Score 176; DB 21; Length 521;
Best Local Similarity	80.7%; Pred. No. 1.6e-20;
Matches 221; Conservative	0; Mismatches 45; Indels 8; Gaps 1;
QY 1321	accgagatcacctcgaaacttgctcccaagttaacgaatttcctcgttcaggctcc 1380
Db 56	ATCTCGGTCACTGCACAACTTGCTGCCAATTCAAGCATTCCTCCGCTCAGCCTCC 115
OY 1381	cgccttagcttggaactacaagcgc-----caagccgcgcgaattttgtattgta 1432
Db 116	TGAGTAGCCAGGATTACAGGTGCCCCGCCACACACCAGCTAATTTTGTATTTTAATA 175
OY 1433	gagatgggttcacccaatatagccgcgcttgcttgtaacctcgaacctcagtgatcca 1492
Db 176	GAGATGGGGTTACTATAGTTGGCCAGAGCTAGTCTTGTAGTCTGAGACTCAGGTGATCCA 235
OY 1493	cccacctaagcctcctaagaatgctgggatatacagaagcatgagttcaacgcgcgccgaccaag 1552
Db 236	CCC GCCCTCAGCCTCCCAAGAAGTCTGGGATTCAGAGCAAGATCAACCGCCCTCGCCCTTTC 295
OY 1553	gtcagtggttaataagagataactggaatggttt 1586
Db 296	CTGACTTTTITAGTGAATCACCAATTCTAAGTGGTAT 329
RESULT 12	
LOCUS	T53829 551 bp mRNA EST 06-FEB-1995
DEFINITION	y8b5d10.s1 StrataGene liver (c937224) Homo sapiens cDNA clone IMAGE:77971 3' similar to contains L1 repetitive element, mRNA sequence.
ACCESSION	T53829
VERSION	T53829.1 GI:655690
KEYWORDS	EST.
SOURCE	human.

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 551) Haller,L., Lennon,G., Becker,M., Donald,M.F., Chiapelli,B., Chissee,S., Dietrich,N., Dubnue,T., Favello,A., Gish,W., Hawkins,M., Hulman,M., Kucaba,T., Leary,M., Le,M., Le,N., Morris,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riklin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thillery,Weg,J., Trevasik,E., Underwood,K., Wohlman,P., Weston,R., Wilson,R. and Marra,M.
TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 760 High quality sequence stops: 380 Source: IMAGE Consortium, LNL This clone is available royalty free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 760 Std Error: 0.00 Seq primer: -21m3 High quality sequence stop: 380.
FEATURES	location/Qualifiers 1..551 /organism="Homo sapiens" /db_xref="GDB:497716" /db_xref="taxon:9606" /clone="IMAGE:77971" /clone_id="Stratagene liver (#937224)" /sex="male" /dev_stage="49 years old" /lab_host="SOLR cells (kanamycin resistant)" /note="Organ: liver; Vector: pluscript SK; Site_1: EcorRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Hepatectomy from normal male caucasian. Average Insert size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3"
BASE COUNT	119 a 134 c 127 g 163 t 8 others
ORIGIN	
Query Match	3.3% Score 176; DB 39; Length 551;
Best Local Similarity	80.7% Pred. No. 1.6e-20;
Matches 221: Conservative	0; Mismatches 45; Indels 8; Gaps 1;
0Y	1321 acctgagctcactgcaacctctccctccagggtcaagaatctctctgctcaagctcc 1380
Db	47 ATCTGGGTCACTGCACTGCACTGCTCTCCAGATCAAGAGGATTCCTCTGCTCAGCTCC 106
0Y	1381 cgcgtagcttgggaactcacaggcg-----cagcccggtctaatttggatatgtagta 1432
Db	107 TGAGTAGCCAGAGATTACAGGTGCCGCCACACACACACACACTAATTTTGTATATTTAGTA 166
0Y	1433 gagaatggggtttcacacatatgaaccgggtgtcttgaacctctgagcccaagtgatcca 1492
Db	167 GAGATGGGGTTTCACTATAGTTTGCCAGAGCTAGTCTTTGACTCTTACCTCAGGTATCCA 226
0Y	1493 cccaccctcaagctctctctaaagtgctgggaattcaaggcatagtcaccgcgcgcgcgaag 1552
Db	227 CCCGCTCAGCCTCCCAAAAGTGCTGGGATTAACAGGATAGTCACCGCCCTTGCGCTTTC 286
0Y	1553 gtccagtggtttaaagaagaaacttgatggtt 1586
Db	287 CTGACTTTTAACTGATCAACATTCTAAGTGAT 320

LOCUS	AC0283440	589 bp	DNA	GSS	27-Apr-1999
DEFINITION	RPc111-7965.TU	RPc11-11	Homo sapiens	genomic clone	RPc11-11-7965, DNA sequence.
ACCESSION	AC0283440				
VERSION	AC0283440.1	GI:3908257			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 589) Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.				
TITLE	Use of human BAC End sequences for Sequence-Ready Map Building				
JOURNAL	Unpublished (1998)				
COMMENT	Other_GSSs: RPc111-7965.TU Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are derived from the human BAC library RPc11-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPac Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.				
FEATURES	Location/Qualifiers				
source	1..589 /organism="Homo sapiens" /db_xref="GDB:7530100" /db_xref="taxon:9606" /clone="RPc11-11-7965" /clone_11b="RPc11-11" /sex="Male" /cell_type="lymphocytes" /note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPc11 Human Male BAC library"				
BASE COUNT	146 a 126 c 136 g 181 t				
ORIGIN					
Query Match	3.3%; Score 175.8; DB 91; Length 589;				
Best Local Similarity	75.7%; Pred. No. 1.7e-20;				
Matches 234; Conservative	0; Mismatches 67; Indels 8; Gaps 1;				
QY	1280 agggatgagggtctgtgtcttaccacttaacctgtatgtcttaccactctgactcaacc 1339				
DB	105 AGAGCTTCTGCTGTGTGCCAGGCCAGGTACAGTACGTGCGATGTCACTCACTCAAC 164				
QY	1340 tctgtctcccaaggttcaagcaattctctgttctgaagctcccggtagcttggaactaa 1399				
DB	165 TCTGACTCTCTGGGTTCAACCAATTCCTCGTTTAGCCCCCGAGTACGTGGGATTACG 224				
QY	1400 ggc-----caagcccgccgcaattttgtatgttgaagtagagaagggtttcacata 1451				
DB	225 GTGCGCTGCCACCATGCTAATTTTGTGATTTTTCACAGATGGGGTTTACACATA 284				
QY	1452 tttagccgggtgtgtcttgaactctgaacctcaagtgatctaccaccaactcaagctctaa 1511				
DB	285 TTGGTCAGGCTGTGTGGAACCTGACCTCATGTGATTCACCCCTTCACGCTCCCAA 344				
QY	1512 gtgtctggagatacaagcatagtaaccgcgcgcgcgcgaaggatcgtgttataagaa 1571				
DB	345 GTGCTGGGGTTTACAGGCGGACACCGTGGTCTGATCCAGGGGTATGTTTATAGAA 404				
QY	1572 taactgaa 1580				
DB	405 TAATCTGCA 413				

RESULT	14
LOCUS	A0474222/c
DEFINITION	A0474222 386 bp DNA GSS 23-Apr-1999 CITBI-EI-2601E18.TR CITBI-EI Homo sapiens genomic clone 2601E18, DNA sequence.
ACCESSION	AQ474222
VERSION	AQ474222.1 GI:4652483
KEYWORDS	GSS.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 386) Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C. Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building Unpublished (1997) Other-GSSs: CITBI-EI-2601E18.TF Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html . Seq primer: M13 Reverse Class: BAC ends.

Db 65 CTTGCTCGTTTGGA 48

Search completed: December 3, 2000, 10:15:10
Job time: 1398 sec